

## SEQUENCE LISTING

&lt;110&gt; Merck &amp; Co., Inc.

<120> Coccidian parasite casein kinase I as a  
chemotherapeutic target for antiprotozoal agents

&lt;130&gt; 21554 PCT

&lt;150&gt; 60/537,094

&lt;151&gt; 2004-01-16

&lt;160&gt; 45

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 2182

&lt;212&gt; DNA

&lt;213&gt; Eimeria tenella

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (715)...(1722)

&lt;400&gt; 1

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tccctgaggg agcgtgcatg tatggtccgg cagccagctt ggtgtcgag cgtacttct 180
tggaagcgag agagactgtg ggagagcgca aatcactcca gccgcttcca ggggagtctg 240
gggaccgcag gacggttgga ggctgcctgc cggcataaac aggaacaagc gcattcttat 300
tcttctgtgg ttgctgagtt ctggctgcgt tcaagggggt tcacctcttc cccttctggc 360
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accggtgcc cggtggccgt cgaaattgaa gcaggatctc tacagtaagg aacaaatcgc 660
gctattttta aggagtgtgt atacttgggg cgttactcgt gagtattgct gatg atg 717
                                         Met
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gac gtc cgt gtg ggg ggt aag tat cgt ttg ggg agg aag att ggg agc 765
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gga tcc ttc ggc gac atc tac ctt ggt acg aac atc tca aca gga gat 813
Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Asn Ile Ser Thr Gly Asp
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gaa gtc gct atc aaa ttg gaa agc gtg cgg tct agg cat cca caa cta 861
Glu Val Ala Ile Lys Leu Glu Ser Val Arg Ser Arg His Pro Gln Leu
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atc tat gaa agc aag ctg tac aaa atc cta acg ggt gga atc gga atc	909
Ile Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Thr Gly Gly Ile Gly Ile	
50 55 60 65	
ccg act ctt tac tgg tat ggg atc gag ggg gat tac aac gtt atg att	957
Pro Thr Leu Tyr Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met Ile	
70 75 80	
att gag ctt ttg ggc ccg tct ctt gag gac ctc ttc agc att tgc aac	1005
Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys Asn	
85 90 95	
aga aag ctt tct ttg aag act gtt ctg atg ctc gcc gac caa atg cta	1053
Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met Leu	
100 105 110	
aat cgt att gag ttc gtc cac agc aga cat ttc atc cat cga gac atc	1101
Asn Arg Ile Glu Phe Val His Ser Arg His Phe Ile His Arg Asp Ile	
115 120 125	
aag cct gac aat ttt ttg atc ggt agg ggc aaa aag atg tcc att gtt	1149
Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Ile Val	
130 135 140 145	
ttt gct atc gac ttt ggc ctc gca aag aag tac aga gat ccc aga aca	1197
Phe Ala Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Arg Thr	
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cag tcc cat att cct tat cga gaa ggg aag aac ctg aca ggt acc gcg	1245
Gln Ser His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr Ala	
165 170 175	
agg tac gcc tct gtg aac acc cac ttg gga ata gaa cag agc agg cgc	1293
Arg Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg Arg	
180 185 190	
gat gat ctg gaa gcg ctc ggc tac gtc tta atg tac ttc aac aga ggt	1341
Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg Gly	
195 200 205	
tcc tta ccc tgg caa gga tta aag gcc act acg aag aaa gat aaa tat	1389
Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys Tyr	
210 215 220 225	
gac aag att atg gag aag aag atg tcc acc cct att gaa gtc ctt tgc	1437
Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu Cys	
230 235 240	
aaa caa ttt cca ttt gag ttt atc aca tat ctg aac tat tgc cgg tct	1485
Lys Gln Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg Ser	
245 250 255	
ctg cga ttc gaa gat cgc ccg gac tat tcc tat ttg aga cgg ttg ttc	1533
Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg Arg Leu Phe	
260 265 270	

aag gat ctt ttc ttc cgt gag gga tac cag tat gac ttt ata ttc gat 1581  
 Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe Asp  
 275 280 285

tgg aca ttt ctg cat gct gag aga gag cgc gag cgt caa aga cga tcg 1629  
 Trp Thr Phe Leu His Ala Glu Arg Glu Arg Glu Arg Gln Arg Arg Ser  
 290 295 300 305

atg gtc aac caa ggc gca gaa tca ggg aac cag tgg aga cga gac gcg 1677  
 Met Val Asn Gln Gly Ala Glu Ser Gly Asn Gln Trp Arg Arg Asp Ala  
 310 315 320

tcg ggc aga gat cca ctt gga cgg ttg cct cag tta gaa ccg taa 1722  
 Ser Gly Arg Asp Pro Leu Gly Arg Leu Pro Gln Leu Glu Pro \*  
 325 330 335

tctcttttacg ggcagattgc cgtacgggtc ttctgctcat tcagtggcag tgccaccgca 1782  
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<210> 2

<211> 335

<212> PRT

<213> Eimeria tenella

<400> 2

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 35 40 45  
 Leu Ile Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Thr Gly Gly Ile Gly  
 50 55 60  
 Ile Pro Thr Leu Tyr Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met  
 65 70 75 80  
 Ile Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys  
 85 90 95  
 Asn Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met  
 100 105 110  
 Leu Asn Arg Ile Glu Phe Val His Ser Arg His Phe Ile His Arg Asp  
 115 120 125  
 Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Ile  
 130 135 140  
 Val Phe Ala Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Arg  
 145 150 155 160  
 Thr Gln Ser His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr  
 165 170 175

Ala Arg Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg  
 180 185 190  
 Arg Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg  
 195 200 205  
 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys  
 210 215 220  
 Tyr Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu  
 225 230 235 240  
 Cys Lys Gln Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg  
 245 250 255  
 Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg Arg Leu  
 260 265 270  
 Phe Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe  
 275 280 285  
 Asp Trp Thr Phe Leu His Ala Glu Arg Glu Arg Glu Arg Gln Arg Arg  
 290 295 300  
 Ser Met Val Asn Gln Gly Ala Glu Ser Gly Asn Gln Trp Arg Arg Asp  
 305 310 315 320  
 Ala Ser Gly Arg Asp Pro Leu Gly Arg Leu Pro Gln Leu Glu Pro  
 325 330 335

&lt;210&gt; 3

&lt;211&gt; 2076

&lt;212&gt; DNA

<213> *Toxoplasma gondii*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (898)...(1872)

&lt;400&gt; 3

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 ccctttctat gcgttgccac ccgtctgcaa gtatcgcgtc tttcgtctca tcagtgattt 180  
 tctttgcgtg tcgcgttcgg gacgcccttt tctctcctca actaactagc agacgtttct 240  
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 tgcaacttgt cgcgccgtcgt tcttcacttc ttctctccca tcctctcgtg actcttcctc 360  
 tcgagaactc tttctgtcga actctcaacc cccacgactg ctgggtttcgt ggccgtcccg 420  
 catgcacctt gtgtcccgcc gccttggcgc aaacaccgcg tttctctgct gtccgcctcc 480  
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 cacgtacact actccacttg ggtgcccacg cgcggcttct gggagacaga gacggtcctc 720  
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 ccctcggcga acgggcgaag ccgccctgtc gcgcgtcgcg actcagctga ggcgacaggc 840  
 ggtcggcggc gtgacctctc tttctttttg cattcggccc tgattgcagc acgaagg atg 900  
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1

gag gtc agg gtc gga ggc aag tac cga ctt ggt cgg aag atc ggc agc 948  
 Glu Val Arg Val Gly Gly Lys Tyr Arg Leu Gly Arg Lys Ile Gly Ser  
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ggg tca ttc ggt gat att tat atc ggt gca aac att ttg acg ggg gat	996
Gly Ser Phe Gly Asp Ile Tyr Ile Gly Ala Asn Ile Leu Thr Gly Asp	
20 25 30	
gag gtg gcg atc aag ttg gag tct atc aag tcg aag cac ccg cag ctg	1044
Glu Val Ala Ile Lys Leu Glu Ser Ile Lys Ser Lys His Pro Gln Leu	
35 40 45	
ctc tat gag tcg aag ctg tac aaa ctg ctg gct ggc ggc att ggg att	1092
Leu Tyr Glu Ser Lys Leu Tyr Lys Leu Leu Ala Gly Gly Ile Gly Ile	
50 55 60 65	
ccc atg gtc cac tgg tac ggc atc gaa gga gac tac aat gtt atg gtt	1140
Pro Met Val His Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met Val	
70 75 80	
atc gac ctt ctc ggc cct tct ctg gag gac ctt ttc agt atc tgc aat	1188
Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys Asn	
85 90 95	
cgc aaa ctc tct ctc aag acg gtg ttg atg ctc gca gac cag atg ctc	1236
Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met Leu	
100 105 110	
aac cgc atc gag ttt gtc cat agc aag aac ttc atc cat cgc gat atc	1284
Asn Arg Ile Glu Phe Val His Ser Lys Asn Phe Ile His Arg Asp Ile	
115 120 125	
aaa ccc gac aac ttc ctc att ggc cgt gga aag aag atg tcc gtc gtc	1332
Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Val Val	
130 135 140 145	
tac atc atc gat ttc ggt ttg gca aag aaa tat cga gac cca aag act	1380
Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Lys Thr	
150 155 160	
cag caa cat atc cca tac agg gaa ggc aag aac cta aca ggc aca gcg	1428
Gln Gln His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr Ala	
165 170 175	
cgt tac gct tcc atc aac acc cac ctg ggg atc gag cag agt cgg cga	1476
Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg Arg	
180 185 190	
gac gac cta gag gcg ctc ggt tac gtt ctc atg tac ttc aat aga ggt	1524
Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg Gly	
195 200 205	
tct ctt ccg tkg cag ggt ctg aag gcg acg acg aag aag gac aaa tac	1572
Ser Leu Pro Xaa Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys Tyr	
210 215 220 225	
gac aag att atg gag aag aaa atg tct act ccc atc gaa att ttg tgc	1620
Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Ile Leu Cys	
230 235 240	

aag cat ttc cca ttc gag ttc atc acc tac ttg aat tac tgc cgg tcc 1668  
 Lys His Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg Ser  
 245 250 255  
 ctg cgc ttc gag gat cgt cct gac tac gca tac ttg cga cgc ctg ttc 1716  
 Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ala Tyr Leu Arg Arg Leu Phe  
 260 265 270  
 aaa gac ttg ttt ttt aga gag gga tat cag tac gac ttc atc ttc gac 1764  
 Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe Asp  
 275 280 285  
 tgg act ttc atc aac acg gag aag gat cgc gcg agt cga aga agc cag 1812  
 Trp Thr Phe Ile Asn Thr Glu Lys Asp Arg Ala Ser Arg Arg Ser Gln  
 290 295 300 305  
 caa gtt tat gtg gaa gac aac cgg caa gtt gag gag aat cag aac gag 1860  
 Gln Val Tyr Val Glu Asp Asn Arg Gln Val Glu Glu Asn Gln Asn Glu  
 310 315 320  
 ttg ccg atg tag ggtggtcggt gtgcggagggc cggcgggggag cgtggagtcc 1912  
 Leu Pro Met \*

gctgagtctg gaagtctgca gactgtgctc tggcactcga cccacttggt tgtgtttccc 1972  
 tcgactcgcg caggtcgagg aaaacagaga cgaacagggt acccaggagt gtttttggtc 2032  
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<210> 4

<211> 324

<212> PRT

<213> Toxoplasma gondii

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 35 40 45  
 Leu Leu Tyr Glu Ser Lys Leu Tyr Lys Leu Leu Ala Gly Gly Ile Gly  
 50 55 60  
 Ile Pro Met Val His Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met  
 65 70 75 80  
 Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys  
 85 90 95  
 Asn Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met  
 100 105 110  
 Leu Asn Arg Ile Glu Phe Val His Ser Lys Asn Phe Ile His Arg Asp  
 115 120 125  
 Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Val  
 130 135 140  
 Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Lys  
 145 150 155 160



Thr Gln Gln His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr  
 165 170 175  
 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg  
 180 185 190  
 Arg Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg  
 195 200 205  
 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys  
 210 215 220  
 Tyr Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Ile Leu  
 225 230 235 240  
 Cys Lys His Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg  
 245 250 255  
 Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ala Tyr Leu Arg Arg Leu  
 260 265 270  
 Phe Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe  
 275 280 285  
 Asp Trp Thr Phe Ile Asn Thr Glu Lys Asp Arg Ala Ser Arg Arg Ser  
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 Glu Leu Pro Met

<210> 5  
 <211> 2373  
 <212> DNA  
 <213> *Toxoplasma gondii*

<220>  
 <221> CDS  
 <222> (119)...(1417)

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 atg gcg cac cat caa gac acc cgc aac cac acg ggg gtc gga ccc tct 166  
 Met Ala His His Gln Asp Thr Arg Asn His Thr Gly Val Gly Pro Ser  
 1 5 10 15  
 tcg tct atc cct ctg aaa gat ttg aag atc gcc ggc gtc tgg aaa atc 214  
 Ser Ser Ile Pro Leu Lys Asp Leu Lys Ile Ala Gly Val Trp Lys Ile  
 20 25 30  
 ggc aga aaa atc gga tcc ggt tcc ttc ggc gac ata tac aaa ggc ctg 262  
 Gly Arg Lys Ile Gly Ser Gly Ser Phe Gly Asp Ile Tyr Lys Gly Leu  
 35 40 45  
 aat tct cag acc ggt cag gag gtg gcg ctg aag gtc gaa agc acc aag 310  
 Asn Ser Gln Thr Gly Gln Glu Val Ala Leu Lys Val Glu Ser Thr Lys  
 50 55 60  
 gcg aag cat ccg cag ttg ctg tac gaa tac aaa ctt ttg aag cat ttg 358  
 Ala Lys His Pro Gln Leu Leu Tyr Glu Tyr Lys Leu Leu Lys His Leu  
 65 70 75 80

cag gga gga acg ggc att gct caa gtg ttc tgt tgc gag act gcg ggc	406
Gln Gly Gly Thr Gly Ile Ala Gln Val Phe Cys Cys Glu Thr Ala Gly	
85 90 95	
gac cat aac atc atg gcc atg gag ttg ctc gga cct tct tta gag gac	454
Asp His Asn Ile Met Ala Met Glu Leu Leu Gly Pro Ser Leu Glu Asp	
100 105 110	
gtc ttc aac ttg tgc aat cgc acc ttc tct ctc aaa acc att ctt ctt	502
Val Phe Asn Leu Cys Asn Arg Thr Phe Ser Leu Lys Thr Ile Leu Leu	
115 120 125	
ctc gcc gac cag ttt ctg caa cgc gtc gag tac atc cac tcc aag aat	550
Leu Ala Asp Gln Phe Leu Gln Arg Val Glu Tyr Ile His Ser Lys Asn	
130 135 140	
ttc att cac aga gat atc aaa cca gat aac ttt ctt ctc ggc ggt gcc	598
Phe Ile His Arg Asp Ile Lys Pro Asp Asn Phe Leu Leu Gly Gly Ala	
145 150 155 160	
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Gly Asn Gln Asn Thr Ile Tyr Val Ile Asp Phe Gly Leu Ala Lys Lys	
165 170 175	
ttt cgc gat ccg aaa acg cac caa cat att ccg tac aga gaa aac aag	694
Phe Arg Asp Pro Lys Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys	
180 185 190	
aat ctc acg gga acg gcg cgc tac gcg tcc atc agt gcg cat ctg ggt	742
Asn Leu Thr Gly Thr Ala Arg Tyr Ala Ser Ile Ser Ala His Leu Gly	
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Ser Glu Gln Ser Arg Arg Asp Asp Leu Glu Ala Val Gly Tyr Val Leu	
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Met Tyr Phe Cys Arg Gly Gly Thr Leu Pro Trp Gln Gly Ile Lys Ala	
225 230 235 240	
aat acc aaa cag gag aag tac cac aag atc atg gag aag aag atg tcg	886
Asn Thr Lys Gln Glu Lys Tyr His Lys Ile Met Glu Lys Lys Met Ser	
245 250 255	
acg ccc gtc gag gtg cta tgc aag gga tat cca agc gaa ttt gcc aca	934
Thr Pro Val Glu Val Leu Cys Lys Gly Tyr Pro Ser Glu Phe Ala Thr	
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Tyr Leu His Tyr Cys Arg Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr	
275 280 285	
gcc tac ctc aag cga ctc ttt cga gat ctc tac atc aaa gag ggc tac	1030
Ala Tyr Leu Lys Arg Leu Phe Arg Asp Leu Tyr Ile Lys Glu Gly Tyr	
290 295 300	



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gat gac agt gac cgc gaa ttc gac tgg aca gtg aaa ctt tcg tcg cgc 1078
Asp Asp Ser Asp Arg Glu Phe Asp Trp Thr Val Lys Leu Ser Ser Arg
305 310 315 320

agt ctc gga ccg cca agc agt cga gcg caa cat gtt tta ctg agt caa 1126
Ser Leu Gly Pro Pro Ser Ser Arg Ala Gln His Val Leu Leu Ser Gln
325 330 335

gac acc cga acg cga ggg aag cgg gag aca gat cga cct gtc gct gcg 1174
Asp Thr Arg Thr Arg Gly Lys Arg Glu Thr Asp Arg Pro Val Ala Ala
340 345 350

cgg agt ggc gac cgc gaa cga gga atc cat ttc agc aac ggg aac gtg 1222
Arg Ser Gly Asp Arg Glu Arg Gly Ile His Phe Ser Asn Gly Asn Val
355 360 365

ggc aat cct tcg atg gca acg aac ccc ggc ggc ctg tca gtc atg gtg 1270
Gly Asn Pro Ser Met Ala Thr Asn Pro Gly Gly Leu Ser Val Met Val
370 375 380

cat gaa cgc acg agt ctg gtg gat cag gga gac cgt ggg tcg cgc gaa 1318
His Glu Arg Thr Ser Leu Val Asp Gln Gly Asp Arg Gly Ser Arg Glu
385 390 395 400

act tct acg cgg aaa gaa gac gcg aag gac ggc aga tgg cca gga ggc 1366
Thr Ser Thr Arg Lys Glu Asp Ala Lys Asp Gly Arg Trp Pro Gly Gly
405 410 415

aga ttt tct tgt ctt cca ctg tta tgt cgg cgc tct ccg acg aag gcc 1414
Arg Phe Ser Cys Leu Pro Leu Leu Cys Arg Arg Ser Pro Thr Lys Ala
420 425 430

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atcgacaatg gatcctagac acgcccgttt aaaatcagag gtattcctaa aaaaaaaaaa 2367
aaaaaa 2373

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&lt;210&gt; 6

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Toxoplasma gondii

&lt;400&gt; 6

Met	Ala	His	His	Gln	Asp	Thr	Arg	Asn	His	Thr	Gly	Val	Gly	Pro	Ser
1				5				10						15	
Ser	Ser	Ile	Pro	Leu	Lys	Asp	Leu	Lys	Ile	Ala	Gly	Val	Trp	Lys	Ile
			20					25					30		
Gly	Arg	Lys	Ile	Gly	Ser	Gly	Ser	Phe	Gly	Asp	Ile	Tyr	Lys	Gly	Leu
		35					40					45			
Asn	Ser	Gln	Thr	Gly	Gln	Glu	Val	Ala	Leu	Lys	Val	Glu	Ser	Thr	Lys
	50					55					60				
Ala	Lys	His	Pro	Gln	Leu	Leu	Tyr	Glu	Tyr	Lys	Leu	Leu	Lys	His	Leu
65					70					75					80
Gln	Gly	Gly	Thr	Gly	Ile	Ala	Gln	Val	Phe	Cys	Cys	Glu	Thr	Ala	Gly
				85					90					95	
Asp	His	Asn	Ile	Met	Ala	Met	Glu	Leu	Gly	Pro	Ser	Leu	Glu	Asp	
			100					105				110			
Val	Phe	Asn	Leu	Cys	Asn	Arg	Thr	Phe	Ser	Leu	Lys	Thr	Ile	Leu	Leu
		115					120					125			
Leu	Ala	Asp	Gln	Phe	Leu	Gln	Arg	Val	Glu	Tyr	Ile	His	Ser	Lys	Asn
	130					135					140				
Phe	Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Phe	Leu	Leu	Gly	Gly	Ala
145					150					155					160
Gly	Asn	Gln	Asn	Thr	Ile	Tyr	Val	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Lys
				165					170					175	
Phe	Arg	Asp	Pro	Lys	Thr	His	Gln	His	Ile	Pro	Tyr	Arg	Glu	Asn	Lys
			180					185					190		
Asn	Leu	Thr	Gly	Thr	Ala	Arg	Tyr	Ala	Ser	Ile	Ser	Ala	His	Leu	Gly
		195					200					205			
Ser	Glu	Gln	Ser	Arg	Arg	Asp	Asp	Leu	Glu	Ala	Val	Gly	Tyr	Val	Leu
	210					215					220				
Met	Tyr	Phe	Cys	Arg	Gly	Gly	Thr	Leu	Pro	Trp	Gln	Gly	Ile	Lys	Ala
225					230					235					240
Asn	Thr	Lys	Gln	Glu	Lys	Tyr	His	Lys	Ile	Met	Glu	Lys	Lys	Met	Ser
				245					250					255	
Thr	Pro	Val	Glu	Val	Leu	Cys	Lys	Gly	Tyr	Pro	Ser	Glu	Phe	Ala	Thr
			260					265					270		
Tyr	Leu	His	Tyr	Cys	Arg	Ser	Leu	Arg	Phe	Glu	Asp	Arg	Pro	Asp	Tyr
		275					280					285			
Ala	Tyr	Leu	Lys	Arg	Leu	Phe	Arg	Asp	Leu	Tyr	Ile	Lys	Glu	Gly	Tyr
	290					295					300				
Asp	Asp	Ser	Asp	Arg	Glu	Phe	Asp	Trp	Thr	Val	Lys	Leu	Ser	Ser	Arg
305					310					315					320
Ser	Leu	Gly	Pro	Pro	Ser	Ser	Arg	Ala	Gln	His	Val	Leu	Leu	Ser	Gln
				325					330					335	
Asp	Thr	Arg	Thr	Arg	Gly	Lys	Arg	Glu	Thr	Asp	Arg	Pro	Val	Ala	Ala
			340					345					350		
Arg	Ser	Gly	Asp	Arg	Glu	Arg	Gly	Ile	His	Phe	Ser	Asn	Gly	Asn	Val
		355					360					365			
Gly	Asn	Pro	Ser	Met	Ala	Thr	Asn	Pro	Gly	Gly	Leu	Ser	Val	Met	Val
	370					375					380				

His Glu Arg Thr Ser Leu Val Asp Gln Gly Asp Arg Gly Ser Arg Glu  
 385 390 395 400  
 Thr Ser Thr Arg Lys Glu Asp Ala Lys Asp Gly Arg Trp Pro Gly Gly  
 405 410 415  
 Arg Phe Ser Cys Leu Pro Leu Leu Cys Arg Arg Ser Pro Thr Lys Ala  
 420 425 430

<210> 7  
 <211> 543  
 <212> DNA  
 <213> Toxoplasma gondii (EST)

<400> 7  
 agaatttcat tcacagagat atcaaaccag ataactttct tctcggcggg gccggcaatc 60  
 aaaacacgat ctacgtgatc gacttcggcc tggcgaagaa gtttcgcgat ccgaaaacgc 120  
 accaacatat tccgtacaga gaaaacaaga atctcacggg aacggcgcgc tacgcgtcca 180  
 tcagtgcgca tctgtgttcc gagcagagtc gccgagatga cctcgaagca gtcgggtacg 240  
 ttctcatgta cttctgtcga ggaggcacgc tgccttggca gggcatcaaa gcgaatacca 300  
 aacaggagaa gtaccacaag atcatggaga agaagatgtc gacgcccgtc gaggtgctat 360  
 gcaagggata tccaagcgaa tttgccacat acttgacta ctgccgtcc ttgcgattcg 420  
 aggaccgacc ggactacgcc tacctcaagc gactctttcg agatctctac atcaaagagg 480  
 gctacgatga cagtgaccgc gaattcgact ggacagtga actttcgtcg cgcagtctcg 540  
 gac 543

<210> 8  
 <211> 341  
 <212> DNA  
 <213> Toxoplasma gondii (EST)

<400> 8  
 gatattcaag cgaatttgcc acatacttgc actactgccg ctctttgcga ttcgaggacc 60  
 gaccggacta cgcctacctc aagcgactct ttcgagatct ctacatcaaa gagggctacg 120  
 atgacagtga ccgcgaatc gactggacag tgaaactttc gtcgcgcagt ctccggaccgc 180  
 caagcagtcg agcgcaacat gttttactga gtcaagacac ccgaacgcga gggaagcggg 240  
 agacagatcg acctgtcgct gtgcggagtg gcgaccgcga acgaggaatc catttcagca 300  
 acgggaacgt gggcaatccc tccgatggca acgaaccccc g 341

<210> 9  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 9  
 gatatcaaac cagataactt tctttctcggc 30

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 10  
caaggagcgg cagtagtgca agt

23

<210> 11  
<211> 21  
<212> PRT  
<213> Eimeria tenella (peptide)

<400> 11  
Ala Lys Asp Leu Ile Arg Lys Met Leu Ala Tyr Val Pro Ser Met Arg  
1 5 10 15  
Ile Ser Ala Arg Asp  
20

<210> 12  
<211> 20  
<212> PRT  
<213> Eimeria tenella (peptide)

<400> 12  
Ala Val Lys Val Ile Ser Lys Arg Gln Val Lys Gln Lys Thr Asp Lys  
1 5 10 15  
Glu Leu Leu Leu  
20

<210> 13  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptide

<400> 13  
Arg Arg Lys Asp Leu His Asp Asp Glu Glu Asp Glu Ala Met Ser Ile  
1 5 10 15  
Thr Ala

<210> 14  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptide

<400> 14  
Arg Arg Ala Asp Asp Ser Asp Asp Asp Asp Asp  
1 5 10

<210> 15  
<211> 15  
<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 15

Pro Leu Ala Arg Thr Leu Ser Val Ala Gly Leu Pro Gly Lys Lys  
1 5 10 15

<210> 16

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 16

Met His Lys Asn Glu Thr Val Glu Cys Leu Lys  
1 5 10

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 17

Asp Asp Asp Glu Glu Ser Ile Thr Arg Arg  
1 5 10

<210> 18

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 18

Leu Arg Arg Ala Ser Leu Gly  
1 5

<210> 19

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 19

Lys Arg Arg Arg Ala Leu Ser Val Ala Ser Leu Pro Gly Leu  
 1 5 10

<210> 20  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptide

<400> 20  
 Arg Arg Arg Glu Glu Glu Thr Glu Glu Glu  
 1 5 10

<210> 21  
 <211> 324  
 <212> PRT  
 <213> Plasmodium falciparum

<400> 21  
 Met Glu Ile Arg Val Ala Asn Lys Tyr Ala Leu Gly Lys Lys Leu Gly  
 1 5 10 15  
 Ser Gly Ser Phe Gly Asp Ile Tyr Val Ala Lys Asp Ile Val Thr Met  
 20 25 30  
 Glu Glu Phe Ala Val Lys Leu Glu Ser Thr Arg Ser Lys His Pro Gln  
 35 40 45  
 Leu Leu Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Gly Gly Gly Ile Gly  
 50 55 60  
 Val Pro Lys Val Tyr Trp Tyr Gly Ile Glu Gly Asp Phe Thr Ile Met  
 65 70 75 80  
 Val Leu Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Thr Leu Cys  
 85 90 95  
 Asn Arg Lys Phe Ser Leu Lys Thr Val Arg Met Thr Ala Asp Gln Met  
 100 105 110  
 Leu Asn Arg Ile Glu Tyr Val His Ser Lys Asn Phe Ile His Arg Asp  
 115 120 125  
 Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Val Thr Leu  
 130 135 140  
 Ile His Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ser Arg  
 145 150 155 160  
 Ser His Thr Ser Tyr Pro Tyr Lys Glu Gly Lys Asn Leu Thr Gly Thr  
 165 170 175  
 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg  
 180 185 190  
 Arg Asp Asp Ile Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Leu Arg  
 195 200 205  
 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ile Ser Lys Lys Asp Lys  
 210 215 220  
 Tyr Asp Lys Ile Met Glu Lys Lys Ile Ser Thr Ser Val Glu Val Leu  
 225 230 235 240  
 Cys Arg Asn Ala Ser Phe Glu Phe Val Thr Tyr Leu Asn Tyr Cys Arg  
 245 250 255  
 Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Thr Tyr Leu Arg Arg Leu  
 260 265 270



Leu Lys Asp Leu Phe Ile Arg Glu Gly Phe Thr Tyr Asp Phe Leu Phe  
 275 280 285  
 Asp Trp Thr Cys Val Tyr Ala Ser Glu Lys Asp Lys Lys Lys Met Leu  
 290 295 300  
 Glu Asn Lys Asn Arg Phe Asp Gln Thr Ala Asp Gln Glu Gly Arg Asp  
 305 310 315 320  
 Gln Arg Asn Asn

<210> 22  
 <211> 353  
 <212> PRT  
 <213> Leshmania major

<400> 22  
 Met Asn Val Glu Leu Arg Val Gly Asn Arg Tyr Arg Ile Gly Gln Lys  
 1 5 10 15  
 Ile Gly Ser Gly Ser Phe Gly Glu Ile Phe Arg Gly Thr Asn Ile Gln  
 20 25 30  
 Thr Gly Asp Pro Val Ala Ile Lys Leu Glu Gln Val Lys Thr Arg His  
 35 40 45  
 Pro Gln Leu Thr Tyr Glu Ser Arg Phe Tyr Arg Ile Leu Gly Ser Gly  
 50 55 60  
 Gly Gly Ala Val Gly Ile Pro Met Met Phe Tyr His Gly Val Glu Gly  
 65 70 75 80  
 Glu Phe Asn Val Met Val Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp  
 85 90 95  
 Leu Phe Ser Phe Cys Gly Arg Arg Leu Ser Leu Lys Thr Thr Leu Met  
 100 105 110  
 Leu Ala Asp Gln Met Ile Ser Arg Ile Glu Phe Val His Ser Lys Ser  
 115 120 125  
 Val Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met Gly Thr Gly  
 130 135 140  
 Lys Lys Gly His His Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys  
 145 150 155 160  
 Tyr Arg Asp Pro Arg Thr His Ala His Ile Pro Tyr Lys Glu Gly Lys  
 165 170 175  
 Ser Leu Thr Gly Thr Ala Arg Tyr Cys Ser Ile Asn Thr His Met Gly  
 180 185 190  
 Val Glu Gln Gly Arg Arg Asp Asp Met Glu Gly Ile Gly Tyr Ile Leu  
 195 200 205  
 Met Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala His  
 210 215 220  
 Thr Lys Gln Glu Lys Tyr Asn Arg Ile Ser Glu Arg Lys Gln Thr Thr  
 225 230 235 240  
 Pro Val Glu Leu Leu Cys Lys Gly Phe Pro Ser Glu Phe Ala Ala Tyr  
 245 250 255  
 Met Asn Tyr Val Arg Ala Leu Arg Phe Glu Asp Lys Pro Asp Tyr Ser  
 260 265 270  
 Tyr Leu Lys Arg Met Phe Arg Asp Leu Phe Val Arg Glu Gly Tyr His  
 275 280 285  
 Val Asp Tyr Val Phe Asp Trp Thr Leu Lys Arg Ile His Glu Ser Leu  
 290 295 300  
 Gln Glu Gln Gln Ser Phe Pro Gly Gly Ser Asn Gly Gly Gly Ala Ala  
 305 310 315 320

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<210> 23
<211> 330
<212> PRT
<213> Trypanosoma cruzi
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- 16 -

<210> 24  
<211> 55  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 24  
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<210> 25  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 25  
cggctctagat cagagggaga cgcgcgctcct gacc 34

<210> 26  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 26  
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<210> 27  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 27  
cggctctagat caaaaaaaga acttacgccc acggcgt 37

<210> 28  
<211> 68  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 28

ggcggatccg aaaatggact acaaagacga tgacgacaag gaggtcaggg tcggaggcaa 60  
gtaccgac 68

<210> 29  
<211> 64  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 29  
ggcgtgatca aaaatggact acaaagacga tgacgacaag gcgcaccatc aagacacccg 60  
caac 64

<210> 30  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 30  
ggcctcgagg gccttcgtcg gagagcgccg acataacagt g 41

<210> 31  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 31  
ggcgtcgacg atgttatggt cgccccgcagt ctcgcaaca 39

<210> 32  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 32  
ggcgtcgacg atcttgtggt acttctcctg tttggtattc gctttgatgc 50

<210> 33  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 33

ggcctcgagc acgttcccgt tgctgaaatg gattcctcgt t

41

<210> 34

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 34

atggactaca aagacgatga cgacaaggac gtccgtgtgg ggggtaagta tcgtttg

57

<210> 35

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 35

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<210> 36

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 36

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gtatcgtttg

60

70

<210> 37

<211> 11

<212> PRT

<213> Eimeria tenella (peptide)

<400> 37

Ser Arg His Pro Gln Leu Ile Tyr Glu Ser Lys

1

5

10

<210> 38

<211> 12

<212> PRT

<213> Eimeria tenella (peptide)

<400> 38

Thr Val Leu Met Leu Ala Asp Gln Met Leu Asn Arg  
1 5 10

<210> 39  
<211> 11  
<212> PRT  
<213> Eimeria tenella (peptide)

<400> 39  
Asp Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg  
1 5 10

<210> 40  
<211> 8  
<212> PRT  
<213> Eimeria tenella (peptide)

<400> 40  
Thr Gln Ser His Ile Pro Tyr Arg  
1 5

<210> 41  
<211> 14  
<212> PRT  
<213> Eimeria tenella (peptide)

<400> 41  
Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg  
1 5 10

<210> 42  
<211> 11  
<212> PRT  
<213> Eimeria tenella (peptide)

<400> 42  
Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg  
1 5 10

<210> 43  
<211> 5  
<212> PRT  
<213> Eimeria tenella (peptide)

<400> 43  
Asp Leu Phe Phe Arg  
1 5

<210> 44  
<211> 30  
<212> DNA  
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<220>  
<223> oligonucleotide



<400> 44  
aaaatggggc agcaggaaag cactcttggg

30

<210> 45  
<211> 29  
<212> DNA  
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<220>  
<223> oligonucleotide

<400> 45  
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29